

1644

P#13

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/248,964A

DATE: 11/28/2000

TIME: 11:56:24

Input Set : A:\HAR005.APP.txt

Output Set: N:\CRF3\11282000\I248964A.raw

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DEC 15 2000

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ENTERED

2 <110> APPLICANT: WUCHERPFENNIG, Kai W
3 STROMINGER, Jack L
5 <120> TITLE OF INVENTION: MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING
6 DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES
7 THEREFOR
9 <130> FILE REFERENCE: HAR-005
11 <140> CURRENT APPLICATION NUMBER: 09/248,964A
12 <141> CURRENT FILING DATE: 1999-02-12
14 <150> PRIOR APPLICATION NUMBER: PCT/US97/14503
15 <151> PRIOR FILING DATE: 1997-08-15
17 <150> PRIOR APPLICATION NUMBER: 60/075,351
18 <151> PRIOR FILING DATE: 1998-02-19
20 <150> PRIOR APPLICATION NUMBER: 60/024,007
21 <151> PRIOR FILING DATE: 1996-08-15
23 <160> NUMBER OF SEQ ID NOS: 14
25 <170> SOFTWARE: PatentIn Ver. 2.0
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30 <213> ORGANISM: Artificial Sequence
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33 <223> OTHER INFORMATION: Description of Artificial Sequence: DR2-Fos fusion
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42 <223> OTHER INFORMATION: 3' end of secretory signal
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45 <221> NAME/KEY: misc_structure
46 <222> LOCATION: (22)..(594)
47 <223> OTHER INFORMATION: DRA*0101 extracellular domain
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52 <223> OTHER INFORMATION: Linker sequence
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57 <223> OTHER INFORMATION: Fos leucine zipper domain
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61 1 5 10 15
63 gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac 96
64 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp

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65          20          25          30
67 ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg 144
68 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
69          35          40          45
71 gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa 192
72 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
73          50          55          60
75 ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg 240
76 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
77 65          70          75          80
79 aca aag cgc tcc aac tat act cgg atc acc aat gta cct cca gag gta 288
80 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
81          85          90          95
83 act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc 336
84 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
85          100          105          110
87 atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg 384
88 Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
89          115          120          125
91 ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc 432
92 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
93          130          135          140
95 ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc ccc ttc 480
96 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
97 145          150          155          160
99 ctg ccc tca act gag gac gtt tac gac tgc agy gtg gag cac tgg ggc 528
100 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
101          165          170          175
103 ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct 576
104 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
105          180          185          190
107 ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat 624
108 Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
109          195          200          205
111 aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg 672
112 Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
113          210          215          220
115 cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc 720
116 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
117 225          230          235          240
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120 Ile Leu Ala Ala His
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125 <212> TYPE: PRT
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128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: DR2-Fos fusion

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131 <220> FEATURE:
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133 <222> LOCATION: (1)..(7)
134 <223> OTHER INFORMATION: 3' end of secretory signal
136 <220> FEATURE:
137 <221> NAME/KEY: misc_structure
138 <222> LOCATION: (8)..(198)
139 <223> OTHER INFORMATION: DRA*0101 extracellular domain
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: (199)..(205)
144 <223> OTHER INFORMATION: linker sequence
146 <220> FEATURE:
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: (206)..(245)
149 <223> OTHER INFORMATION: Fos leucine zipper domain
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153 1 5 10 15
155 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
156 20 25 30
158 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
159 35 40 45
161 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
162 50 55 60
164 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
165 65 70 75 80
167 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
168 85 90 95
170 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
171 100 105 110
172 Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
173 115 120 125
175 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
176 130 135 140
178 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
179 145 150 155 160
181 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
182 165 170 175
184 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
185 180 185 190
187 Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Leu Thr Asp
188 195 200 205
190 Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
191 210 215 220
193 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
194 225 230 235 240
196 Ile Leu Ala Ala His
197 245

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209 <222> LOCATION: (1)..(756)
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214 <223> OTHER INFORMATION: 3' end of secretory signal
216 <220> FEATURE:
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219 <223> OTHER INFORMATION: DRB1*1501 extracellular domain
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223 <222> LOCATION: (616)..(636)
224 <223> OTHER INFORMATION: Linker sequence
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234 1 5 10 15
236 cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg 96
237 Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
238 20 25 30
240 ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac 144
241 Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
242 35 40 45
244 agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac 192
245 Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
246 50 55 60
248 gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc 240
249 Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
250 65 70 75 80
252 gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc 288
253 Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
254 85 90 95
256 aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag 336
257 Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
258 100 105 110
260 acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt 384
261 Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly

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262          115          120          125
264 ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa 432
265 Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
266          130          135          140
268 gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg 480
269 Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
270 145          150          155          160
272 acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag 528
273 Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
274          165          170          175
276 gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca 576
277 Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
278          180          185          190
280 gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga 624
281 Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
282          195          200          205
286 ggt ggc ggc ggt cgc atc gcc cgg ctg gag gaa aaa gtg aaa acc ttg 672
287 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
288          210          215          220
290 aaa gct cag aac tcg gaq ctc gcg tcc acg gcc aac atg ctc agg gaa 720
291 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
292 225          230          235          240
294 cag gtg gca cag ctt aaa cag aaa gtc atg aac cat/tgagaattct atgac 771
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296          245          250
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299 <211> LENGTH: 252
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301 <213> ORGANISM: Artificial Sequence
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304 <223> OTHER INFORMATION: Description of Artificial Sequence: DR2-Jun fusion
306 <220> FEATURE:
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308 <222> LOCATION: (1)..(7)
309 <223> OTHER INFORMATION: 3' end of secretory signal
311 <220> FEATURE:
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313 <222> LOCATION: (8)..(205)
314 <223> OTHER INFORMATION: DRB1*1501 extracellular domain
316 <220> FEATURE:
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318 <222> LOCATION: (206)..(212)
319 <223> OTHER INFORMATION: Linker sequence
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322 <221> NAME/KEY: misc_feature
323 <222> LOCATION: (213)..(252)
324 <223> OTHER INFORMATION: Jun leucine zipper domain
326 <400> SEQUENCE: 4
327 Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp

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VERIFICATION SUMMARY DATE: 11/28/2000
PATENT APPLICATION: US/09/248,964A TIME: 11:56:25

Input Set : A:\HAR005.APP.txt
Output Set: N:\CRF3\11282000\I248964A.raw

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